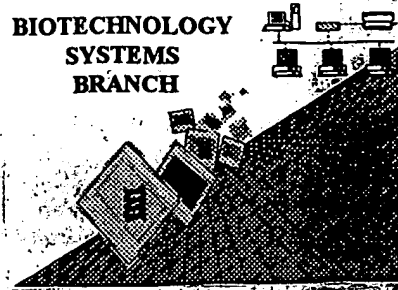


0280

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/026,952  
Source: OPE  
Date Processed by STIC: 1/14/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**  
**VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER:

10/026 952

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000  
    *correct format*
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s) 26 missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

## RAW SEQUENCE LISTING

DATE: 01/14/2002

PATENT APPLICATION: US/10/026,952

TIME: 18:49:59

Input Set : A:\seqlist-0942 4980006 ascii

Output Set: N:\CRF3\01142002\J026952.raw

5 <110> APPLICANT: Nazarenko, Irina  
 7 Rashtchian, Ayoub  
 9 Solus, Joseph  
 11 Pires, Richard M.  
 13 Darfler, Marlene  
 15 Gebeyehu, Gulilat  
 17 Astatke, Mekbib  
 21 <120> TITLE OF INVENTION: Primers and Methods for the Detection and Discrimination of  
 Nucleic  
 22 Acids  
 26 <130> FILE REFERENCE: 0942.4980006  
 30 <140> CURRENT APPLICATION NUMBER: US/10/026,952  
 30 <141> CURRENT FILING DATE: 2001-12-27  
 30 <150> PRIOR APPLICATION NUMBER: 60/330,468  
 32 <151> PRIOR FILING DATE: 2001-10-23  
 36 <150> PRIOR APPLICATION NUMBER: 60/139,890  
 38 <151> PRIOR FILING DATE: 1999-06-22  
 42 <150> PRIOR APPLICATION NUMBER: 60/175,959  
 44 <151> PRIOR FILING DATE: 2000-01-13  
 48 <150> PRIOR APPLICATION NUMBER: 09/599,594  
 50 <151> PRIOR FILING DATE: 2000-06-22  
 54 <150> PRIOR APPLICATION NUMBER: 09/748,146  
 56 <151> PRIOR FILING DATE: 2000-12-27  
 60 <160> NUMBER OF SEQ ID NOS: 139  
 64 <170> SOFTWARE: PatentIn version 3.1  
 68 <210> SEQ ID NO: 1  
 70 <211> LENGTH: 23  
 72 <212> TYPE: DNA  
 74 <213> ORGANISM: Artificial Sequence  
 78 <220> FEATURE:  
 80 <223> OTHER INFORMATION: Primer  
 82 <220> FEATURE:  
 84 <221> NAME/KEY: misc\_feature  
 86 <222> LOCATION: (18)..(18)  
 88 <223> OTHER INFORMATION: Fluorescently labeled  
 92 <400> SEQUENCE: 1  
 93 ccttctcatg gtggctgtag aac  
 96 <210> SEQ ID NO: 2  
 98 <211> LENGTH: 23  
 100 <212> TYPE: DNA  
 102 <213> ORGANISM: Artificial Sequence  
 106 <220> FEATURE:  
 108 <223> OTHER INFORMATION: Primer  
 110 <220> FEATURE:  
 112 <221> NAME/KEY: misc\_feature  
 114 <222> LOCATION: (1)..(1)  
 116 <223> OTHER INFORMATION: Fluorescently labeled  
 120 <400> SEQUENCE: 2

PP. 3, 4, 6

23

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/026,952

DATE: 01/14/2002

TIME: 18:49:59

Input Set : A:\seqlist-0942 4980006 ascii

Output Set: N:\CRF3\01142002\J026952.raw

```

121 ccttctcatg gtggctgtag aac 23
124 <210> SEQ ID NO: 3
126 <211> LENGTH: 23
128 <212> TYPE: DNA
130 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
136 <223> OTHER INFORMATION: Primer
138 <400> SEQUENCE: 3 23
139 ggtctacagc caccatgaga agg
142 <210> SEQ ID NO: 4
144 <211> LENGTH: 23
146 <212> TYPE: DNA
148 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
154 <223> OTHER INFORMATION: Primer
156 <400> SEQUENCE: 4 23
157 ggggctgcga ctgtgctccg gca
160 <210> SEQ ID NO: 5
162 <211> LENGTH: 23
164 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
172 <223> OTHER INFORMATION: Primer
174 <400> SEQUENCE: 5 23
175 tgccggagca cagtcgcagc ccc
178 <210> SEQ ID NO: 6
180 <211> LENGTH: 20
182 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
190 <223> OTHER INFORMATION: Primer
192 <220> FEATURE:
194 <221> NAME/KEY: misc_feature
196 <222> LOCATION: (1)..(1)
198 <223> OTHER INFORMATION: Fluorescently labeled
202 <400> SEQUENCE: 6 20
203 aataatagga tgaggcagga
206 <210> SEQ ID NO: 7
208 <211> LENGTH: 20
210 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
218 <223> OTHER INFORMATION: Primer
220 <220> FEATURE:
222 <221> NAME/KEY: misc_feature
224 <222> LOCATION: (1)..(1)
226 <223> OTHER INFORMATION: Labeled with BODIPY 530/550
230 <400> SEQUENCE: 7 20
231 aataatagga tgaggcagga

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/026,952

DATE: 01/14/2002

TIME: 18:49:59

Input Set : A:\seqlist-0942 4980006 ascii

Output Set: N:\CRF3\01142002\J026952.raw

234 <210> SEQ ID NO: 8  
236 <211> LENGTH: 20  
238 <212> TYPE: DNA  
240 <213> ORGANISM: Artificial Sequence  
244 <220> FEATURE:  
246 <223> OTHER INFORMATION: Primer  
248 <400> SEQUENCE: 8  
249 tcctgcctca tcctattatt 20  
252 <210> SEQ ID NO: 9  
254 <211> LENGTH: 23  
256 <212> TYPE: DNA  
258 <213> ORGANISM: Artificial Sequence  
262 <220> FEATURE:  
264 <223> OTHER INFORMATION: Primer  
266 <400> SEQUENCE: 9 23  
267 gagttgaccg taacagacat ctt  
270 <210> SEQ ID NO: 10  
272 <211> LENGTH: 24  
274 <212> TYPE: DNA  
276 <213> ORGANISM: Artificial Sequence  
280 <220> FEATURE:  
282 <223> OTHER INFORMATION: Primer  
284 <400> SEQUENCE: 10 24  
285 ggcattgccg acaggatgta gaag  
288 <210> SEQ ID NO: 11  
290 <211> LENGTH: 18  
292 <212> TYPE: DNA  
294 <213> ORGANISM: Artificial Sequence  
298 <220> FEATURE:  
300 <223> OTHER INFORMATION: Primer  
302 <400> SEQUENCE: 11 18  
303 gggccggact cgtcatac  
306 <210> SEQ ID NO: 12  
308 <211> LENGTH: 28  
310 <212> TYPE: DNA  
312 <213> ORGANISM: Artificial Sequence  
316 <220> FEATURE:  
318 <223> OTHER INFORMATION: Primer  
320 <400> SEQUENCE: 12 28  
321 ggttgtagag cactcagcac aatgaaga  
324 <210> SEQ ID NO: 13  
326 <211> LENGTH: 23  
328 <212> TYPE: DNA  
330 <213> ORGANISM: Artificial Sequence  
334 <220> FEATURE:  
336 <223> OTHER INFORMATION: Primer  
338 <400> SEQUENCE: 13  
W--> 339 000  
342 <210> SEQ ID NO: 14

*incorrect format for  
an intentionally skipped  
sequence (see item 8 on  
Error Summary  
Sheet)*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/026,952

DATE: 01/14/2002

TIME: 18:49:59

Input Set : A:\seqlist-0942 4980006 ascii

Output Set: N:\CRF3\01142002\J026952.raw

```

344 <211> LENGTH: 23
346 <212> TYPE: DNA
348 <213> ORGANISM: Artificial Sequence
352 <220> FEATURE:
354 <223> OTHER INFORMATION: Primer
356 <400> SEQUENCE: 14
357 ccttctcatg gtggctgtag aac
360 <210> SEQ ID NO: 15
362 <211> LENGTH: 23
364 <212> TYPE: DNA
366 <213> ORGANISM: Artificial Sequence
370 <220> FEATURE:
372 <223> OTHER INFORMATION: Primer
374 <400> SEQUENCE: 15
375 ccttctcatg gtggctgtag aat
378 <210> SEQ ID NO: 16
380 <211> LENGTH: 24
382 <212> TYPE: DNA
384 <213> ORGANISM: Artificial Sequence
388 <220> FEATURE:
390 <223> OTHER INFORMATION: Primer
392 <400> SEQUENCE: 16
393 gtgtccttct catgggtggct gtag
396 <210> SEQ ID NO: 17
398 <211> LENGTH: 24
400 <212> TYPE: DNA
402 <213> ORGANISM: Artificial Sequence
406 <220> FEATURE:
408 <223> OTHER INFORMATION: Primer
410 <400> SEQUENCE: 17
411 gtgtccttct catgggtggct gtag
414 <210> SEQ ID NO: 18
416 <211> LENGTH: 23
418 <212> TYPE: DNA
420 <213> ORGANISM: Artificial Sequence
424 <220> FEATURE:
426 <223> OTHER INFORMATION: Primer
428 <400> SEQUENCE: 18
W--> 429 000
432 <210> SEQ ID NO: 19
434 <211> LENGTH: 23
436 <212> TYPE: DNA
438 <213> ORGANISM: Artificial Sequence
442 <220> FEATURE:
444 <223> OTHER INFORMATION: Primer
446 <220> FEATURE:
448 <221> NAME/KEY: misc_feature
450 <222> LOCATION: (18)..(18)
452 <223> OTHER INFORMATION: Fluorescently labeled

```

*Sum 8* → The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/026,952

DATE: 01/14/2002

TIME: 18:49:59

Input Set : A:\seqlist-0942 4980006 ascii

Output Set: N:\CRF3\01142002\J026952.raw

```

456 <400> SEQUENCE: 19
457 ccttctcatg gtggctgtag aat 23
460 <210> SEQ ID NO: 20
462 <211> LENGTH: 24
464 <212> TYPE: DNA
466 <213> ORGANISM: Artificial Sequence
470 <220> FEATURE:
472 <223> OTHER INFORMATION: Primer
474 <220> FEATURE:
476 <221> NAME/KEY: misc_feature
478 <222> LOCATION: (22)..(22)
480 <223> OTHER INFORMATION: Fluorescently labeled
484 <400> SEQUENCE: 20
485 gtgtccttct catgggtggct gtag 24
488 <210> SEQ ID NO: 21
490 <211> LENGTH: 24
492 <212> TYPE: DNA
494 <213> ORGANISM: Artificial Sequence
498 <220> FEATURE:
500 <223> OTHER INFORMATION: Primer
502 <220> FEATURE:
504 <221> NAME/KEY: misc_feature
506 <222> LOCATION: (22)..(22)
508 <223> OTHER INFORMATION: Fluorescently labeled
512 <400> SEQUENCE: 21
513 gtgtccttct catgggtggct gtat 24
516 <210> SEQ ID NO: 22
518 <211> LENGTH: 25
520 <212> TYPE: DNA
522 <213> ORGANISM: Artificial Sequence
526 <220> FEATURE:
528 <223> OTHER INFORMATION: Primer
530 <220> FEATURE:
532 <221> NAME/KEY: misc_feature
534 <222> LOCATION: (23)..(23)
536 <223> OTHER INFORMATION: Labeled with fluoroscein
540 <400> SEQUENCE: 22
541 ctaccgggtg tctgtgtctc ggtag 25
544 <210> SEQ ID NO: 23
546 <211> LENGTH: 20
548 <212> TYPE: DNA
550 <213> ORGANISM: Artificial Sequence
554 <220> FEATURE:
556 <223> OTHER INFORMATION: Primer
558 <400> SEQUENCE: 23
559 cgtacctggc tatctgtgtc 20
562 <210> SEQ ID NO: 24
564 <211> LENGTH: 20
566 <212> TYPE: DNA

```

10/026,95

6

<210> 26

<211> 22

<212> DNA

<213> Artificial

*see item 11 on Eno Summary Sheet*

<400> 26

aacacacctg gctatctgtg tt

22

*PSI*

Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.



VERIFICATION SUMMARY

PATENT APPLICATION: US/10/026,952

DATE: 01/14/2002

TIME: 18:50:00

Input Set : A:\seqlist-0942 4980006 ascii

Output Set: N:\CRF3\01142002\J026952.raw

L:30 M:270 C: Current Application Number differs, Replaced Current Application No  
 L:30 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:339 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (13) SEQUENCE:  
 L:429 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:  
 L:604 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26  
 L:608 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:608 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:1015 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (48) SEQUENCE:  
 L:1033 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (49) SEQUENCE:  
 L:1051 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (50) SEQUENCE:  
 L:1469 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (71) SEQUENCE:  
 L:1771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85  
 L:1929 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:92  
 L:1947 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (93) SEQUENCE:  
 L:2021 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (96) SEQUENCE:  
 L:2299 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (107) SEQUENCE:  
 L:2317 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (108) SEQUENCE:  
 L:2443 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (115) SEQUENCE:  
 L:2543 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (120) SEQUENCE:  
 L:2561 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (121) SEQUENCE:  
 L:2633 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (125) SEQUENCE:  
 L:2715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:129  
 L:2771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:131  
 L:2881 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (136) SEQUENCE:  
 L:2899 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (137) SEQUENCE:  
 L:2917 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (138) SEQUENCE: